

# Introduction of Avian Influenza A(H6N5) Virus into Asia from North America by Wild Birds

## Appendix

**Appendix Table.** Isolates sharing the highest nucleotide identity with each segment of A/Mandarin duck/Korea/K17-1638-5/2017(H6N5) found in GenBank database on April 15, 2019.

Gene*	Strain name	GenBank accession no.	nt identity
PB2	A/glaucous-winged gull/Southcentral Alaska/16MB03648/2016(H5N2)	CY239407.1	99%
PB1	A/American black duck/Maryland/16OS2661/2017(H7N3)	MK236794.1	99%
PA	A/mallard/Alberta/71/2017(H3N8)	MH411975.1	99%
HA	A/northern pintail/California/HS052B/2015(H6N5)	KY983161.1	99%
NP	A/American green-winged teal/Missouri/17OS3212/2017(H3N8)	MK236738.1	99%
NA	A/American wigeon/California/HS010/2015(H12N5)	KY983225.1	98%
M	A/mallard/Alberta/390/2017(H1N1)	MH637401.1	99%
NS	A/northern pintail/Alaska/16-041335-6/2016(H5N2)	MH546895.1	99%

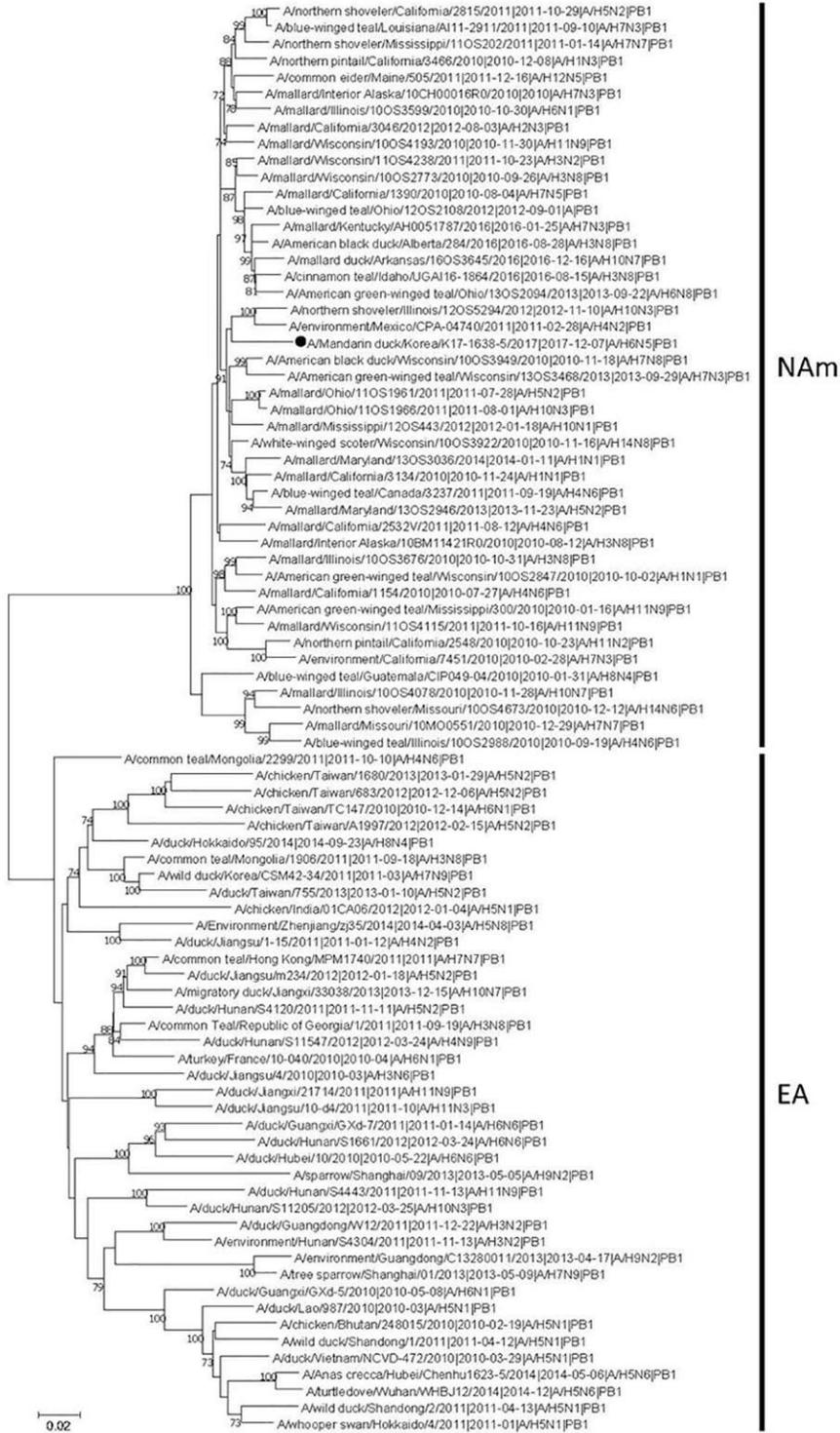
\*HA, hemagglutinin; M, matrix; NA, neuraminidase; NP, nucleoprotein; NS, nonstructural; PA, polymerase acidic; PB, polymerase basic



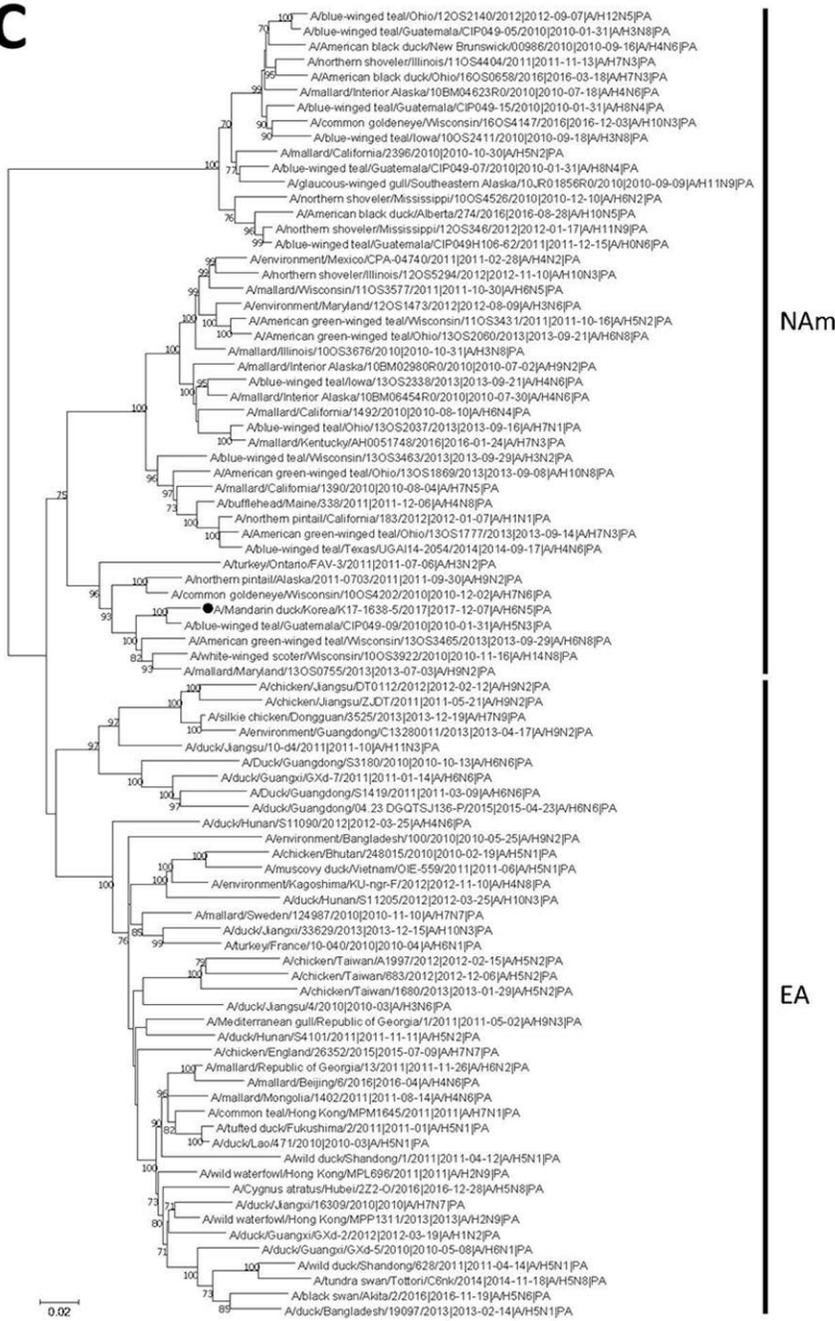
**Appendix Figure 1.** Sampling location of A/Mandarin duck/Korea/K17-1638-5/2017(H6N5) virus (indicated with red circle) in South Korea. Map was retrieved from Google Maps (2019 June 28), <https://www.google.com/maps/@37.7003952,126.6354144,74246m/data=!3m1!1e3!5m1!1e4?hl=en>.



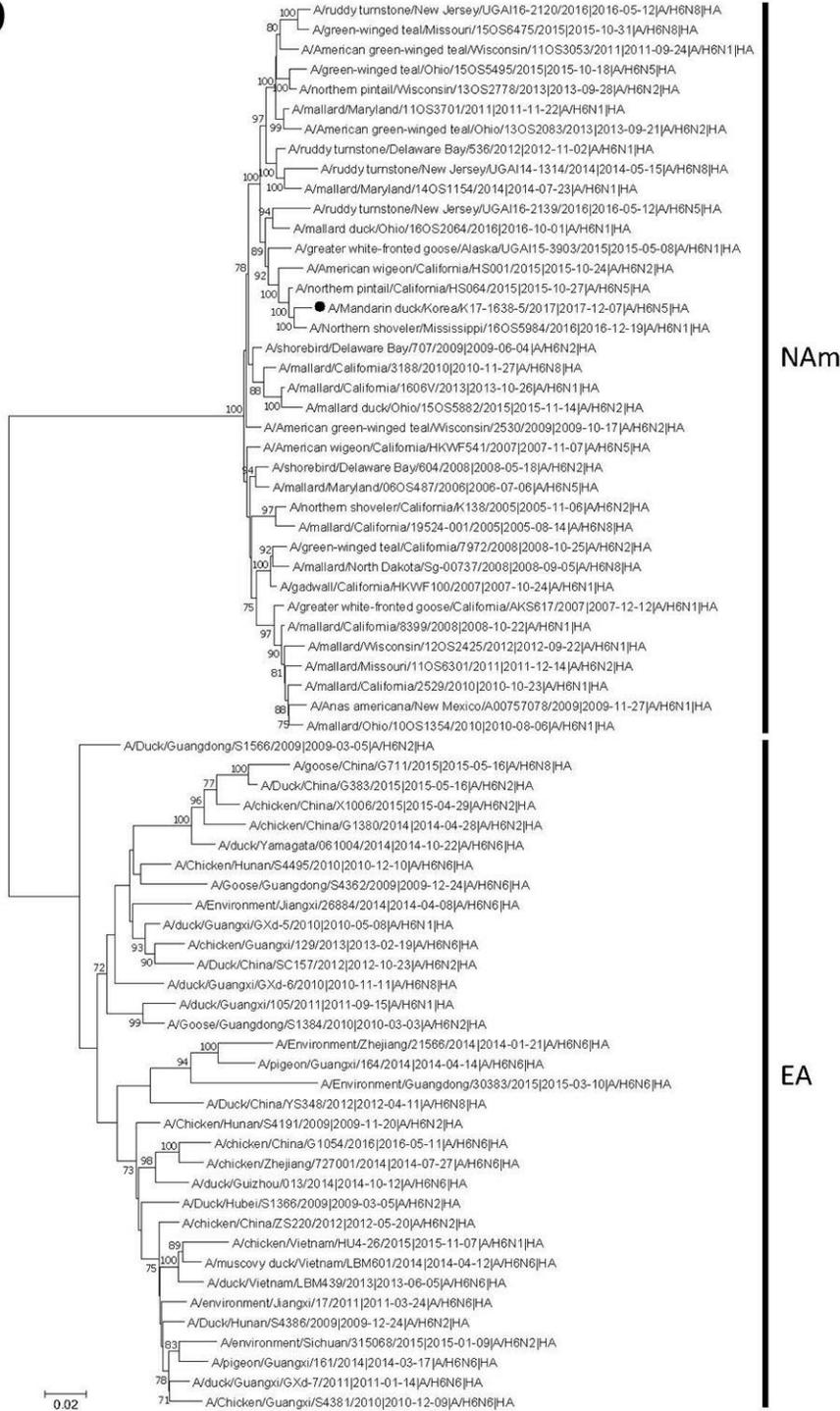
B



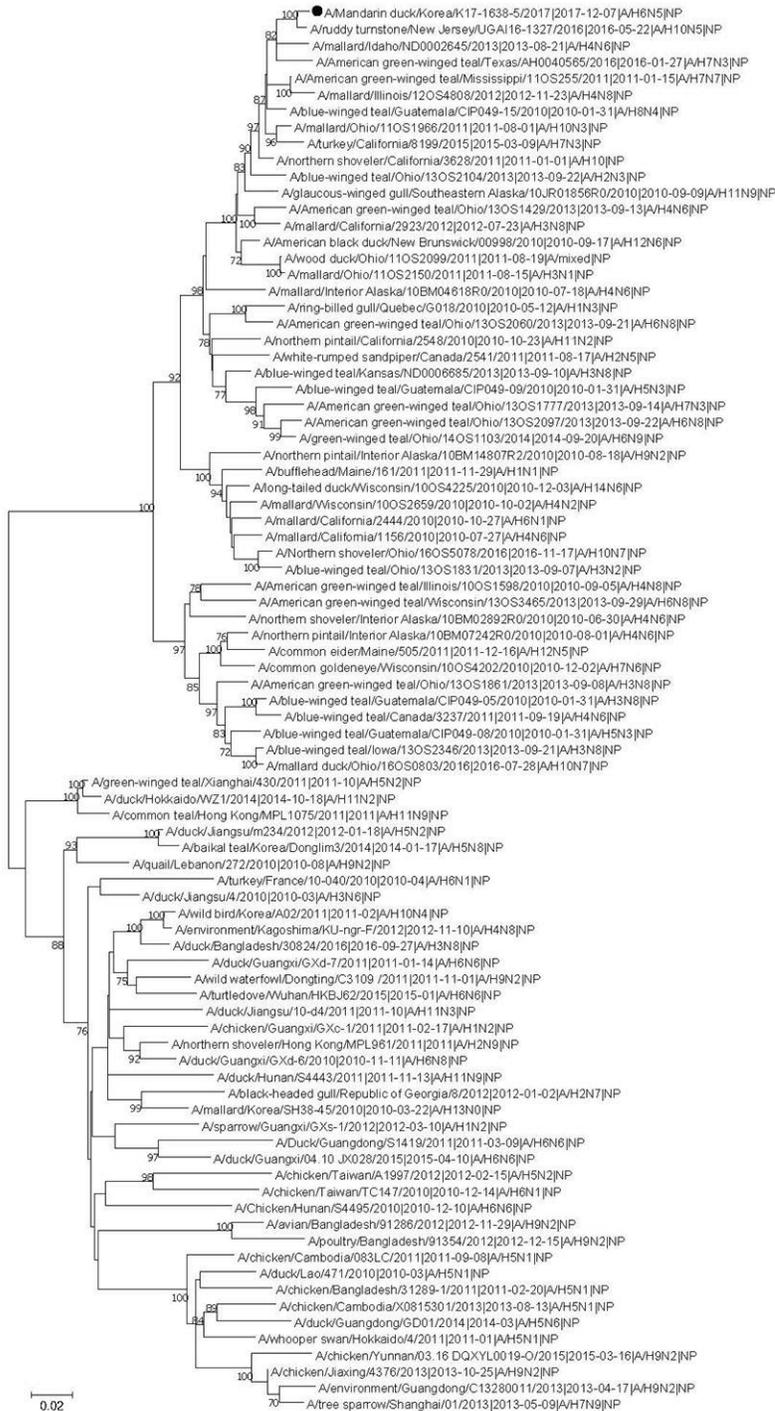
C



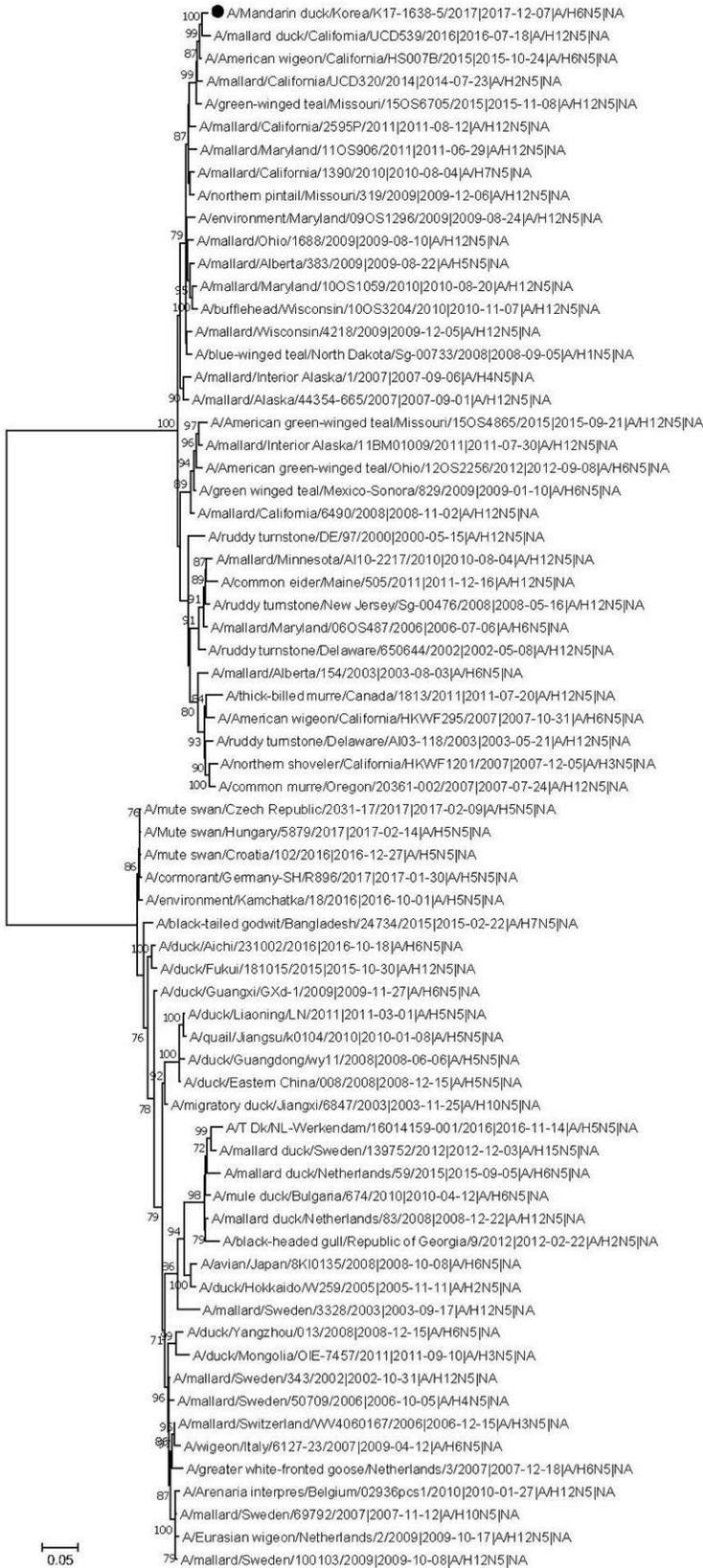
D



E



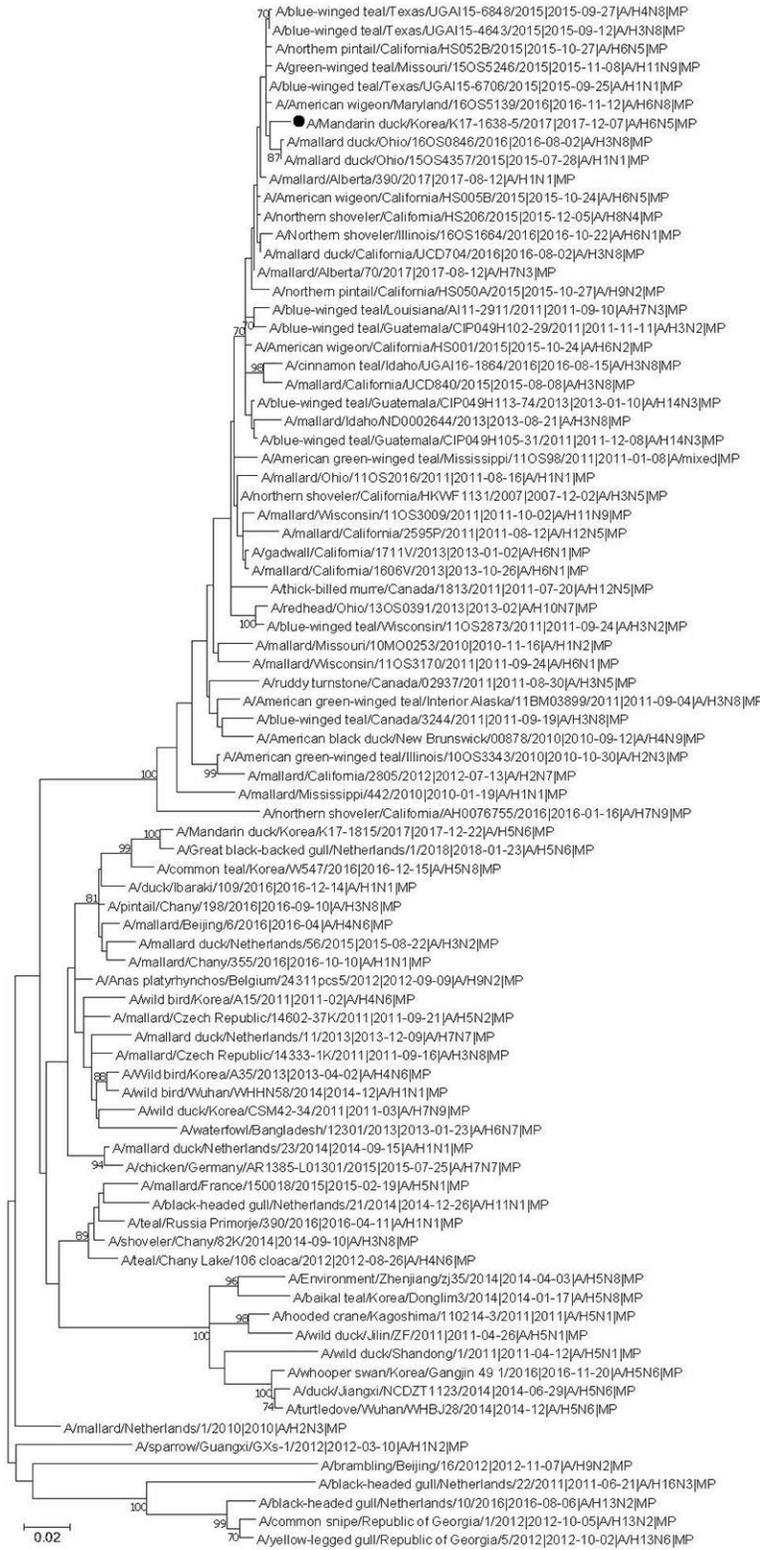
F



NAm

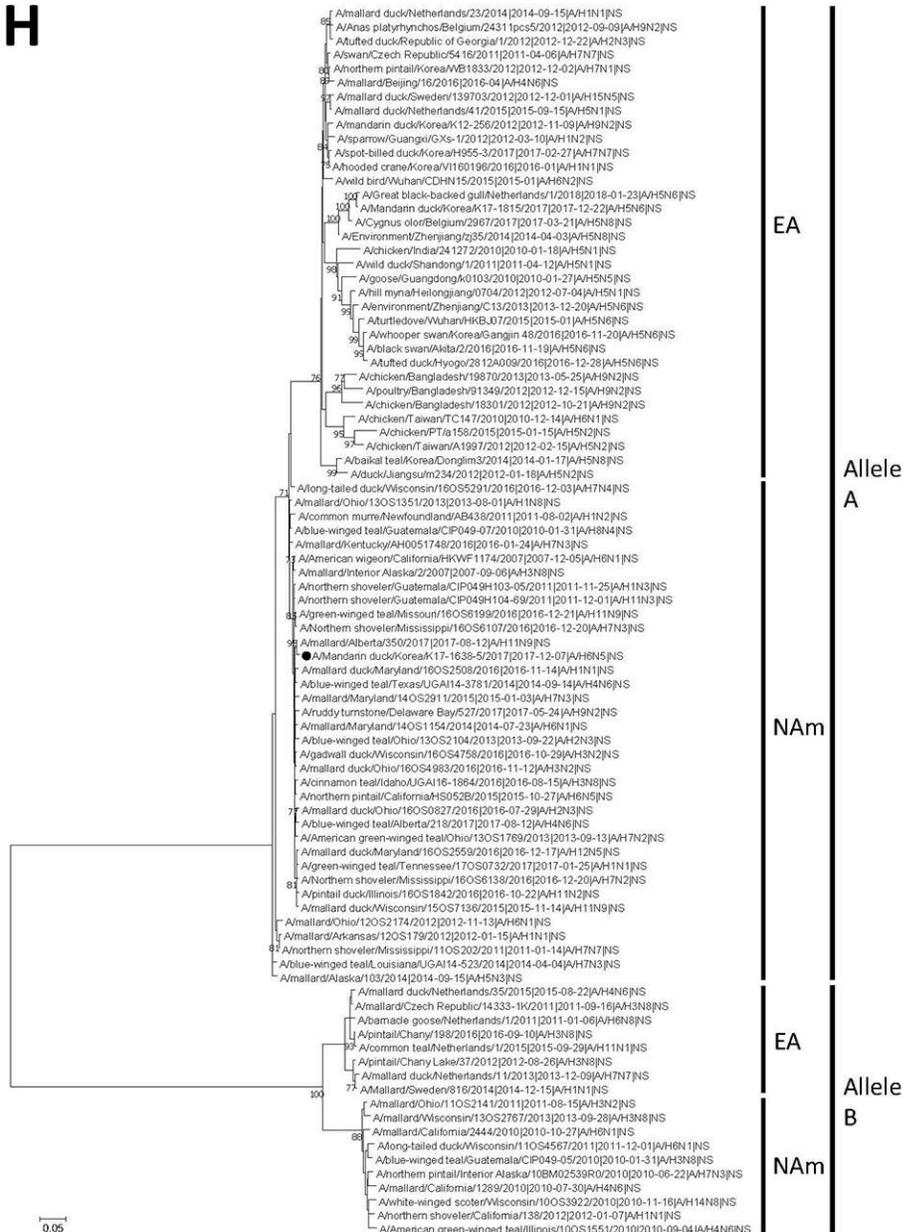
EA

G



NAm

EA

**H**

**Appendix Figure 2.** Maximum-likelihood phylogenetic trees for the reference strains of Eurasian (EA) and North American (NA) lineages and A/Mandarin duck/Korea/K17-1638-5/2017(H6N5) virus (indicated with black circle). Bootstrap values >70% are shown. A) Polymerase basic 2 gene; B) polymerase basic 1 gene; C) polymerase acidic gene; D) hemagglutinin gene; E) nucleoprotein gene; F) neuraminidase gene; G) matrix gene; H) nonstructural gene.